

## WEST Search History

DATE: Tuesday, June 15, 2004

Hide?	Set Name	Query	Hit Count
		<i>DB=PGPB; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L5	20030108538.pn. and lipase	1
<input type="checkbox"/>	L4	20030108538.pn. and lipg	0
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L3	L2 and l1	2
<input type="checkbox"/>	L2	endothelial adj lipase	8
<input type="checkbox"/>	L1	lipg	878

END OF SEARCH HISTORY

09/277401  
STN Search Summary

=> d his

FILE 'CAPLUS' ENTERED AT 15:13:48 ON 15 JUN 2004

L1 127 S ENDOTHELIAL (2W)LIPASE  
L2 17 S LIPG  
L3 135 S L1 OR L2  
L4 57 S L3 AND (CHOLESTEROL OR APOPLIPOPROTEIN)  
L5 25 S L4 AND HUMAN  
L6 36 S L4 AND PD<2000

L6 ANSWER 1 OF 36 CAPLUS COPYRIGHT 2004 ACS on STN

AN 1999:216824 CAPLUS

TI A novel endothelial-derived lipase that modulates HDL metabolism

AU Jaye, Michael; Lynch, Kevin J.; Krawiec, John; Marchadier, Dawn; Maugeais, Cyrille; Doan, Kim; South, Victoria; Amin, Dilip; Perrone, Mark; Rader, Daniel J.

SO Nature Genetics (1999), 21(4), 424-428

L6 ANSWER 4 OF 36 CAPLUS COPYRIGHT 2004 ACS on STN

AN 1998:171862 CAPLUS

TI Lipoprotein metabolism

AU Beisiegel, U.

SO European Heart Journal (1998), 19(Suppl. A), A20-A23

DT Journal; General Review

L6 ANSWER 5 OF 36 CAPLUS COPYRIGHT 2004 ACS on STN

AN 1997:54344 CAPLUS

TI Relationship of plasma cholesteryl ester transfer protein to HDL cholesterol. Studies in normotriglyceridemia and moderate hypertriglyceridemia

AU Foeger, Bernhard; Ritsch, Andreas; Doblinger, Alfred; Wessels, Holger; Patsch, Josef R.

SO Arteriosclerosis, Thrombosis, and Vascular Biology (1996), 16(12), 1430-1436

OM protein - protein search, using sw model

Run on: April 30, 2004, 08:01:57 ; Search time 59 Seconds  
(without alignments)  
2394.470 Million cell updates/sec

Title: US-09-277-401A-8  
Perfect score: 2709  
Sequence: 1 MSNSVPLLCFWSLCYCFAAG.....RKCRDGWRMKNETSPTVELP 500  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1586107 seqs, 282547505 residues  
Total number of hits satisfying chosen parameters: 1586107  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2709	100.0	500	2 AAW59792	Aaw59792 Amino aci
2	2709	100.0	500	2 AAY23759	Aay23759 Human end
3	2709	100.0	500	3 AAB19178	Aab19178 Human LIP
4	2709	100.0	500	5 AAO14635	Aao14635 Human lip
5	2709	100.0	500	6 ABU03569	Abu03569 Angiogene
6	2709	100.0	500	6 ABR64225	Abr64225 Angiogene
7	2709	100.0	500	7 ADE38385	Ade38385 Human pro
8	2350	86.7	440	7 ADE47728	Ade47728 Human NOV
9	2195	81.0	500	2 AAY23760	Aay23760 <u>Mouse</u> end
10	1872	69.1	345	2 AAW59793	Aaw59793 Amino aci
11	1872	69.1	345	3 AAB19179	Aab19179 The catal
12	1872	69.1	353	2 AAW59790	Aaw59790 Amino aci
13	1872	69.1	353	3 AAB19176	Aab19176 A partial
14	1872	69.1	354	2 AAW59791	Aaw59791 Amino aci

Applicant's

in IDS  
12/17/97

→ First 345aa

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OM protein - protein search, using sw model

Run on: April 30, 2004, 08:03:37 ; Search time 20 Seconds  
(without alignments)  
2404.788 Million cell updates/sec

Title: US-09-277-401A-8  
Perfect score: 2709  
Sequence: 1 MSNSVPLLCFWSLCYCFAAG.....RKCRDGWRMKNETSPTVELP 500

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1227.5	45.3	490	1	S04331	chicken lipoprotein lipase
2	1164	43.0	450	1	A27053	lipoprotein lipase
3	1164	43.0	475	2	JC4242	lipoprotein lipase
4	1164	43.0	478	2	S29846	lipoprotein lipase
5	1161	42.9	475	1	LIHUL	lipoprotein lipase
6	1160	42.8	474	1	JH0790	lipoprotein lipase
7	1159	42.8	474	1	A40570	lipoprotein lipase
8	1148	42.4	478	2	S18158	lipoprotein lipase
9	1140	42.1	465	1	A27330	lipoprotein lipase
10	1095.5	40.4	510	2	S15893	triacylglycerol li
11	1065	39.3	499	2	A28997	triacylglycerol li
12	1050.5	38.8	494	2	A27442	triacylglycerol li
13	574	21.2	457	2	I48206	triacylglycerol li
14	547.5	20.2	465	2	C43357	triacylglycerol li

OM protein - protein search, using sw model

Run on: April 30, 2004, 08:02:31 ; Search time 17 Seconds  
(without alignments)  
1531.475 Million cell updates/sec

Title: US-09-277-401A-8  
Perfect score: 2709  
Sequence: 1 MSNSVPLLCFWSLCYCFAAG.....RKCRDGWRMKNETSPTVELP 500

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2709	100.0	500	1	LIPE_HUMAN
2	2207	81.5	500	1	LIPE_MOUSE
3	1227.5	45.3	490	1	LIPL_CHICK
4	1164	43.0	465	1	LIPL_BOVIN
5	1164	43.0	475	1	LIPL_PAPAN
6	1164	43.0	478	1	LIPL_SHEEP
7	1161	42.9	474	1	LIPL_MOUSE
8	1161	42.9	475	1	LIPL_HUMAN
9	1160	42.8	474	1	LIPL_RAT
10	1158	42.7	475	1	LIPL_MUSVI
11	1156	42.7	478	1	LIPL_FELCA
12	1148	42.4	478	1	LIPL_PIG
13	1140	42.1	465	1	LIPL_CAVPO
14	1088.5	40.2	510	1	LIPH_MOUSE
15	1067	39.4	499	1	LIPH_HUMAN
16	1045.5	38.6	494	1	LIPH_RAT
17	574	21.2	457	1	LIPP_MYOCO
18	547.5	20.2	465	1	LIPP_HUMAN

1999  
GenBank → Q9y5x9 homo sapien  
Q9wvg5 mus musculu  
P11602 gallus gall  
P11151 bos taurus  
P49060 papio anubi  
Q29524 ovis aries  
P11152 mus musculu  
P06858 homo sapien  
Q06000 rattus norv  
O46647 mustela vis  
P55031 felis silve  
P49923 sus scrofa  
P11153 cavia porce  
P27656 mus musculu  
P11150 homo sapien  
P07867 rattus norv  
Q64425 myocastor c  
P16233 homo sapien

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OM protein - protein search, using sw model

Run on: April 30, 2004, 08:03:07 ; Search time 46 Seconds  
(without alignments)  
3429.546 Million cell updates/sec

Title: US-09-277-401A-8  
Perfect score: 2709  
Sequence: 1 MSNSVPLLCFWSLCYCFAAG.....RKCRDGWRMKNETSPTVELP 500

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertibrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1524.5	56.3	500	13	Q803Y3	Q803y3 brachydanio
2	1310.5	48.4	511	13	Q98UI3	Q98ui3 pagrus majo
3	1308.5	48.3	510	13	Q98UI2	Q98ui2 pagrus majo
4	1212.5	44.8	490	13	Q9PSV4	Q9psv4 gallus gall
5	1164	43.0	449	6	Q95KN9	Q95kn9 macaca fasc

OM protein - protein search, using sw model

Run on: April 30, 2004, 08:04:37 ; Search time 22 Seconds  
(without alignments)  
1173.318 Million cell updates/sec

Title: US-09-277-401A-8  
Perfect score: 2709  
Sequence: 1 MSNSVPLLCFWSLCYCFAAG.....RKCRDGWRMKNETSPTVELP 500

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	2709	100.0	500	4	US-08-985-492-8	Sequence 8, Appli	
2	1872	69.1	345	4	US-08-985-492-10	Sequence 10, Appl	
3	1872	69.1	353	4	US-08-985-492-4	Sequence 4, Appli	
4	1872	69.1	354	4	US-08-985-492-6	Sequence 6, Appli	
5	1128.5	41.7	472	4	US-08-985-492-13	Sequence 13, Appl	
6	1067	39.4	499	4	US-08-985-492-14	Sequence 14, Appl	
7	555	20.5	473	4	US-09-411-132A-7	Sequence 7, Appli	
8	547.5	20.2	465	4	US-08-985-492-15	Sequence 15, Appl	
9	547.5	20.2	465	4	US-09-411-132A-6	Sequence 6, Appli	
10	537	19.8	467	4	US-09-411-132A-4	Sequence 4, Appli	
11	534	19.7	473	4	US-09-411-132A-8	Sequence 8, Appli	
12	531	19.6	469	4	US-09-411-132A-5	Sequence 5, Appli	

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OM protein - protein search, using sw model

Run on: April 30, 2004, 08:06:17 ; Search time 50 Seconds  
(without alignments)  
2771.896 Million cell updates/sec

Title: US-09-277-401A-8  
Perfect score: 2709  
Sequence: 1 MSNSVPLLCFWSLCYCFAAG.....RKCRDGW RMKNETSPTVELP 500

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.



## SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	2709	100.0	500	12	US-10-211-462-229	Sequence 229, App	
2	2709	100.0	500	14	US-10-128-449A-8 - DIV	Sequence 8, Appli	
3	2709	100.0	500	14	US-10-354-358-46	Sequence 46, Appl	
4	2350	86.7	440	15	US-10-210-130-90	Sequence 90, Appl	
5	1872	69.1	345	14	US-10-128-449A-10	Sequence 10, Appl	
6	1872	69.1	353	14	US-10-128-449A-4	Sequence 4, Appli	
7	1872	69.1	354	9	US-09-978-295A-178	Sequence 178, App	
8	1872	69.1	354	9	US-09-978-697-178	Sequence 178, App	
9	1872	69.1	354	9	US-09-978-192A-178	Sequence 178, App	
10	1872	69.1	354	9	US-09-999-832A-178	Sequence 178, App	
11	1872	69.1	354	10	US-09-978-189-178	Sequence 178, App	
12	1872	69.1	354	10	US-09-978-608A-178	Sequence 178, App	
13	1872	69.1	354	10	US-09-978-585A-178	Sequence 178, App	
14	1872	69.1	354	10	US-09-978-191A-178	Sequence 178, App	
15	1872	69.1	354	10	US-09-978-403A-178	Sequence 178, App	
16	1872	69.1	354	10	US-09-978-564A-178	Sequence 178, App	
17	1872	69.1	354	10	US-09-999-833A-178	Sequence 178, App	
18	1872	69.1	354	10	US-09-981-915A-178	Sequence 178, App	
19	1872	69.1	354	10	US-09-978-824-178	Sequence 178, App	
20	1872	69.1	354	10	US-09-918-585A-178	Sequence 178, App	
21	1872	69.1	354	10	US-09-978-423A-178	Sequence 178, App	
22	1872	69.1	354	10	US-09-978-193A-178	Sequence 178, App	
23	1872	69.1	354	10	US-09-999-830A-178	Sequence 178, App	
24	1872	69.1	354	10	US-09-978-757A-178	Sequence 178, App	
25	1872	69.1	354	10	US-09-978-187B-178	Sequence 178, App	
26	1872	69.1	354	10	US-09-978-643A-178	Sequence 178, App	
27	1872	69.1	354	10	US-09-978-375A-178	Sequence 178, App	
28	1872	69.1	354	10	US-09-978-298A-178	Sequence 178, App	
29	1872	69.1	354	10	US-09-978-188A-178	Sequence 178, App	
30	1872	69.1	354	10	US-09-978-681A-178	Sequence 178, App	
31	1872	69.1	354	10	US-09-978-194A-178	Sequence 178, App	
32	1872	69.1	354	10	US-09-999-829A-178	Sequence 178, App	
33	1872	69.1	354	10	US-09-978-299A-178	Sequence 178, App	
34	1872	69.1	354	10	US-09-978-544A-178	Sequence 178, App	
35	1872	69.1	354	10	US-09-978-665A-178	Sequence 178, App	
36	1872	69.1	354	10	US-09-978-802A-178	Sequence 178, App	
37	1872	69.1	354	12	US-10-147-493-400	Sequence 400, App	
38	1872	69.1	354	12	US-10-164-749A-178	Sequence 178, App	
39	1872	69.1	354	12	US-10-145-127-400	Sequence 400, App	
40	1872	69.1	354	12	US-10-160-503-400	Sequence 400, App	
41	1872	69.1	354	12	US-10-143-118-400	Sequence 400, App	
42	1872	69.1	354	12	US-10-144-993-400	Sequence 400, App	
43	1872	69.1	354	12	US-10-158-787-400	Sequence 400, App	
44	1872	69.1	354	12	US-09-999-831A-178	Sequence 178, App	
45	1872	69.1	354	12	US-10-140-024-400	Sequence 400, App	

## ALIGNMENTS

RESULT 1  
US-10-211-462-229

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OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 18:01:11 ; Search time 9672 Seconds  
(without alignments)  
11494.508 Million cell updates/sec

Title: US-09-277-401A-7  
Perfect score: 2565  
Sequence: 1 GAATTCGCGGCCGCGTCGAC.....GTCGACGCGGCCGCGAATTC 2565

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*

```

28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	%					Description
	No.	Score	Query Match	Length	ID	
	1	2565	100.0	2565	6	AR371822 Sequence
	2	2565	100.0	2565	6	BD064531 LLG polyp
	3	2525.2	98.4	3927	9	AF118767 Homo sapi
	4	2522	98.3	4150	9	BC060825 Homo sapi
	5	1271.6	49.6	1382	6	AR371820 Sequence
	6	1271.6	49.6	1382	6	BD064529 LLG polyp
	7	1261.6	49.2	1510	6	AX047644 Sequence
	8	1261.6	49.2	1510	6	AX055423 Sequence
	9	1261.6	49.2	1510	6	AX464266 Sequence
	10	1261.6	49.2	1510	9	AY358928 Homo sapi
	11	1177	45.9	3610	10	BC020991 Mus muscu
	12	1140.4	44.5	2227	10	AF118768 Mus muscu
	13	1039.6	40.5	1065	6	AR371821 Sequence
	14	1039.6	40.5	1065	6	BD064530 LLG polyp
	15	1035	40.4	1035	6	AR371823 Sequence
	16	1035	40.4	1035	6	BD064532 LLG polyp
	17	944.2	36.8	2323	9	AK125344 Homo sapi
	18	815.2	31.8	3547	9	AK124636 Homo sapi
c	19	815.2	31.8	198586	9	AC091170 Homo sapi
c	20	813.6	31.7	190119	2	AP001814 Homo sapi
	21	619	24.1	4141	5	BC060756 Xenopus l
	22	525.6	20.5	2258	5	BC044146 Danio rer
	23	425.6	16.6	2946	5	AB054062 Pagrus ma
	24	399.8	15.6	2067	6	BD249917 50 human
	25	398.4	15.5	2328	5	GGLPL X14670 Chicken mRN
	26	396.8	15.5	2297	5	AB016987 Gallus ga
	27	358.8	14.0	1904	5	BC064296 Danio rer
c	28	357.6	13.9	218528	2	AC068829 Homo sapi
	29	357.2	13.9	1744	10	GPILPPL M15483 Guinea pig
	30	357	13.9	1612	9	HSLIPAS X54516 Human mRNA
	31	357	13.9	1924	9	HSLPLR X14390 Human mRNA
	32	357	13.9	2385	9	AK092286 Homo sapi
	33	357	13.9	3549	6	AX334735 Sequence

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OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 17:58:50 ; Search time 928 Seconds  
(without alignments)  
11742.056 Million cell updates/sec

Title: US-09-277-401A-7  
Perfect score: 2565  
Sequence: 1 GAATTCGCGGCCGCGTCGAC.....GTCGACGCGGCCGCGAATTC 2565

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	ID	Description	
1	2565	100.0	2565	2	AAV41622	Aav41622 Nucleotid	
2	2565	100.0	2565	3	AAA96940	Aaa96940 cDNA enco	
3	2525.2	98.4	3927	7	ABX08853	Abx08853 Angiogene	
4	2525.2	98.4	3927	7	ACF34500	Acf34500 Gene enco	
5	2525.2	98.4	3927	9	ADE38384	Ade38384 Human pro	
6	1735	67.6	1755	2	AAX85838	Aax85838 cDNA enco	
7	1714.2	66.8	3638	7	ABX63493	Abx63493 Human cDN	
8	1503	58.6	1503	6	ABL91801	Abl91801 Human lip	

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OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 19:12:11 ; Search time 201 Seconds  
(without alignments)  
7081.836 Million cell updates/sec

Title: US-09-277-401A-7  
Perfect score: 2565  
Sequence: 1 GAATTCGCGGCCGCGTCGAC.....GTCGACGCGGCCGGAATTC 2565

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	% Query		Match Length DB	ID	Description
	Score				
1	2565	100.0	2565	4	US-08-985-492-7
2	1271.6	49.6	1382	4	US-08-985-492-3
3	1039.6	40.5	1065	4	US-08-985-492-5
4	1035	40.4	1035	4	US-08-985-492-9
5	174.4	6.8	225	4	US-08-985-492-11
6	140.6	5.5	367	4	US-08-985-492-1
7	104.2	4.1	9734	3	US-09-347-114A-80
8	81.2	3.2	231	3	US-08-905-124-4
9	74.6	2.9	1401	4	US-09-411-132A-2
10	74.6	2.9	2352	4	US-09-411-132A-1
11	42	1.6	1050	1	US-08-180-209B-16
12	42	1.6	1050	1	US-08-385-745-16

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OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 22:19:02 ; Search time 1024 Seconds  
(without alignments)  
11330.747 Million cell updates/sec

Title: US-09-277-401A-7  
Perfect score: 2565  
Sequence: 1 GAATTCGCGGCCGCGTCGAC.....GTCGACGCGGCCGCGAATTC 2565

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2936184 seqs, 2261732022 residues

Total number of hits satisfying chosen parameters: 5872368

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	2565	100.0	2565	15	US-10-128-449A-7	Sequence 7, Appli
2	2525.2	98.4	3927	13	US-10-211-462-228	Sequence 228, App
3	2525.2	98.4	3927	13	US-10-342-887-1234	Sequence 1234, Ap
4	2525.2	98.4	3927	13	US-10-172-118-1234	Sequence 1234, Ap
5	2525.2	98.4	3927	15	US-10-354-358-45	Sequence 45, Appl
6	2514.2	98.0	4315	15	US-10-133-013-213	Sequence 213, App
7	1714.2	66.8	3638	14	US-10-044-090-493	Sequence 493, App
8	1271.6	49.6	1382	15	US-10-128-449A-3	Sequence 3, Appli
9	1261.6	49.2	1510	9	US-09-978-295A-177	Sequence 177, App
10	1261.6	49.2	1510	9	US-09-978-697-177	Sequence 177, App
11	1261.6	49.2	1510	9	US-09-978-192A-177	Sequence 177, App
12	1261.6	49.2	1510	9	US-09-999-832A-177	Sequence 177, App
13	1261.6	49.2	1510	10	US-09-978-189-177	Sequence 177, App
14	1261.6	49.2	1510	10	US-09-978-608A-177	Sequence 177, App
15	1261.6	49.2	1510	10	US-09-978-585A-177	Sequence 177, App
16	1261.6	49.2	1510	10	US-09-978-191A-177	Sequence 177, App
17	1261.6	49.2	1510	10	US-09-978-403A-177	Sequence 177, App
18	1261.6	49.2	1510	10	US-09-978-564A-177	Sequence 177, App
19	1261.6	49.2	1510	10	US-09-999-833A-177	Sequence 177, App
20	1261.6	49.2	1510	10	US-09-981-915A-177	Sequence 177, App
21	1261.6	49.2	1510	10	US-09-978-824-177	Sequence 177, App
22	1261.6	49.2	1510	10	US-09-918-585A-177	Sequence 177, App
23	1261.6	49.2	1510	10	US-09-978-423A-177	Sequence 177, App
24	1261.6	49.2	1510	10	US-09-978-193A-177	Sequence 177, App
25	1261.6	49.2	1510	10	US-09-999-830A-177	Sequence 177, App
26	1261.6	49.2	1510	10	US-09-978-757A-177	Sequence 177, App
27	1261.6	49.2	1510	10	US-09-978-187B-177	Sequence 177, App
28	1261.6	49.2	1510	10	US-09-978-643A-177	Sequence 177, App
29	1261.6	49.2	1510	10	US-09-978-375A-177	Sequence 177, App
30	1261.6	49.2	1510	10	US-09-978-298A-177	Sequence 177, App
31	1261.6	49.2	1510	10	US-09-978-188A-177	Sequence 177, App
32	1261.6	49.2	1510	10	US-09-978-681A-177	Sequence 177, App
33	1261.6	49.2	1510	10	US-09-978-194A-177	Sequence 177, App
34	1261.6	49.2	1510	10	US-09-999-829A-177	Sequence 177, App
35	1261.6	49.2	1510	10	US-09-978-299A-177	Sequence 177, App
36	1261.6	49.2	1510	10	US-09-978-544A-177	Sequence 177, App
37	1261.6	49.2	1510	10	US-09-978-665A-177	Sequence 177, App
38	1261.6	49.2	1510	10	US-09-978-802A-177	Sequence 177, App
39	1261.6	49.2	1510	13	US-10-147-493-399	Sequence 399, App
40	1261.6	49.2	1510	13	US-10-164-749A-177	Sequence 177, App
41	1261.6	49.2	1510	13	US-10-145-127-399	Sequence 399, App
42	1261.6	49.2	1510	13	US-10-160-503-399	Sequence 399, App
43	1261.6	49.2	1510	13	US-10-143-118-399	Sequence 399, App
44	1261.6	49.2	1510	13	US-10-144-993-399	Sequence 399, App
45	1261.6	49.2	1510	13	US-10-158-787-399	Sequence 399, App

## ALIGNMENTS

RESULT 1  
US-10-128-449A-7

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OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 19:09:51 ; Search time 5886 Seconds  
(without alignments)  
13013.336 Million cell updates/sec

Title: US-09-277-401A-7  
Perfect score: 2565  
Sequence: 1 GAATTCGCGGCCGCGTCGAC.....GTCGACGCGGCCGGAATTC 2565

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gssl:\*



29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result			%				DB	ID	Description
	No.	Score	Match	Length	Query				
	1	1123	43.8	3789	11	AK090224		AK090224	Mus muscu
	2	913.4	35.6	1201	9	AL548592		AL548592	AL548592
	3	891.2	34.7	1144	9	AL550034		AL550034	AL550034
	4	840.4	32.8	907	13	BX459178		BX459178	BX459178
	5	752.8	29.3	868	14	CD642638		CD642638	AGENCOURT
	6	748.4	29.2	824	9	AL548839		AL548839	AL548839
	7	710.4	27.7	929	9	AL553511		AL553511	AL553511
	8	640.4	25.0	651	13	BX474974		BX474974	DKFZp686L
	9	623	24.3	624	13	BX482946		BX482946	DKFZp686N
	10	603.2	23.5	639	13	BX475048		BX475048	DKFZp686D
	11	529.4	20.6	560	13	BX475130		BX475130	DKFZp686M
c	12	501	19.5	614	12	BG997133		BG997133	MR4-HT107
	13	500	19.5	554	13	BX504607		BX504607	DKFZp686D
	14	494.2	19.3	675	13	BU702838		BU702838	UI-M-FC0-
	15	464.4	18.1	961	14	CB992673		CB992673	AGENCOURT
	16	463	18.1	474	9	AA449893		AA449893	zx37dl2.r
	17	459	17.9	481	13	BX110491		BX110491	BX110491
	18	442.2	17.2	596	9	AV616502		AV616502	AV616502
c	19	425.4	16.6	563	9	AI651337		AI651337	wb05a06.x
	20	420.6	16.4	545	12	BM089759		BM089759	503598 MA
	21	416.6	16.2	467	13	BX485783		BX485783	DKFZp686J
	22	408.8	15.9	564	14	CD552788		CD552788	B0349B04-
	23	403.8	15.7	713	13	BU473097		BU473097	603762387
	24	402	15.7	845	13	BU114220		BU114220	603131384
c	25	397.4	15.5	535	9	AI653726		AI653726	wb36f07.x
	26	388.6	15.2	523	14	CD549741		CD549741	B0301E04-
	27	378.2	14.7	512	14	CD553260		CD553260	B0357B11-
c	28	374.4	14.6	512	10	BE502020		BE502020	hy11c07.x
	29	358.2	14.0	1114	14	CD500735		CD500735	CDA46-G02
c	30	358	14.0	369	12	BI056082		BI056082	RC5-GN028
	31	355.4	13.9	1427	29	AY410289		AY410289	Homo sapi
	32	349.4	13.6	1424	29	AY410291		AY410291	Mus muscu
	33	342.6	13.4	1141	14	CD503877		CD503877	CDA64-G10
	34	341.4	13.3	1950	11	AK086023		AK086023	Mus muscu
	35	341.4	13.3	2018	11	AK045064		AK045064	Mus muscu
	36	341.4	13.3	2018	11	AK079446		AK079446	Mus muscu
	37	341.4	13.3	2054	11	AK002645		AK002645	Mus muscu
	38	339.8	13.2	1899	11	AK017272		AK017272	Mus muscu
	39	338.4	13.2	428	10	BF606443		BF606443	273487 MA
c	40	338.4	13.2	476	10	AW594725		AW594725	hg66g09.x
	41	337.6	13.2	828	10	BF100744		BF100744	601754370
	42	325.2	12.7	685	9	AU139929		AU139929	AU139929
	43	310.2	12.1	738	13	BU613137		BU613137	UI-M-EW0-
	44	310.2	12.1	741	14	CB525312		CB525312	UI-M-FY0-
	45	294.2	11.5	1427	29	AY410290		AY410290	Pan trogl